

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2005, 11:07:01 ; Search time 156 Seconds
(without alignments)
45.991 Million cell updates/sec

Title: US-10-827-083-4

Perfect score: 105

Sequence: 1 CDSTLRCLVCQSTHVDIRTLE 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	5 AAUI0804	Aui0804 Human pap
2	105	100.0	30	2 AAR15575	Aar15575 Immunopep
3	105	100.0	30	2 AAW93290	Aaw93290 Human pap
4	105	100.0	50	6 AAO16632	Aao16632 Human pap
5	105	100.0	92	7 ADF74305	Adf74305 Human pap
6	105	100.0	98	2 AAR22767	Aar22767 HPV E7 pe
7	105	100.0	98	2 AAR42361	Aar42361 Human pap
8	105	100.0	98	2 AAW46886	Aaw46886 Amino aci
9	105	100.0	98	2 AAY08020	Aay08020 Human pap
10	105	100.0	98	3 AAY58474	Aay58474 Human pap
11	105	100.0	98	3 AAY50703	Aay50703 HPV16 E7
12	105	100.0	98	3 AAY57721	Aay57721 Human pap
13	105	100.0	98	4 AAB98421	Aab98421 Human pap
14	105	100.0	98	4 AAU01718	Aau01718 Human pap
15	105	100.0	98	4 AAU72607	Aau72607 Human pap
16	105	100.0	98	4 AAB67546	Aab67546 Amino aci
17	105	100.0	98	4 AAB49453	Aab49453 HPV 16E7
18	105	100.0	98	4 AAB31607	Aab31607 Amino aci
19	105	100.0	98	4 AAB86332	Aab86332 HPV 16 E7
20	105	100.0	98	5 AAU77713	Aau77713 Human pap
21	105	100.0	98	5 AAU10810	Aau10810 Human pap
22	105	100.0	98	5 ABB82375	Abb82375 Wild-type
23	105	100.0	98	6 AAO22639	Aao22639 HPV-16 pr
24	105	100.0	98	6 AAO16630	Aao16630 Human pap
25	105	100.0	98	7 ADF09516	Adf09516 Human pap

ALIGNMENTS

RESULT 1

AAUI0804

ID AAUI0804 standard; peptide; 20 AA.

XX AC AAUI0804;

XX DT 29-AUG-2003 (revised)

DT 14-FEB-2002 (first entry)

XX DE Human papillomavirus (HPV) 16 E7 coding region derived peptide #2.

XX KW Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma;

KW adenocarcinoma; koilocytosis; hyperkeratosis; intraepithelial neoplasia;

KW intraepithelial lesion; dysplasia; head cancer; neck cancer;

KW small cell lung cancer; melanoma; oncogene.

XX OS Human papillomavirus type 16.

XX PN WO200177142-A1.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US011233.

XX PR 05-APR-2000; 2000US-0194796P.

XX PA (IMPA-) IMPACT DIAGNOSTICS INC.

XX PI Hu YK;

XX DR WPI; 2002-010888/01.

XX PT New peptides derived from E2, E6 or E7 early coding regions of human

papillomavirus 16 and 18, useful in diagnosis of human papillomavirus

infection and associated malignancy e.g. cervical carcinoma.

XX PS Claim 2; Fig 3; 28pp; English.

CC The invention describes a novel peptide derived from the E2, E6 or E7
early coding region of human papillomavirus (HPV) 16 and 18, which is
soluble in aqueous solution and has a lysine or cysteine residue near the
amino terminus, very few tryptophan, methionine and cysteine residues,
and/or many glycine and asparagine residues. The peptides and diagnostic
method are used to diagnose HPV infection, especially infection with
oncogenic HPV by using peptides derived from the E2 region, since HPV 16
and 18 are the main HPV genetic types associated with cancers, and
presence of antibodies to E2 protein is known to provide evidence of HPV
infection. They are also useful to diagnose HPV associated malignancy or

Adf18635 Human pap
Adf18632 Human pap
Adl190076 Human pap
Adm32916 Amino aci
Ado44073 Amino aci
Adn49005 Human pap
Abb81111 HPV E7 an
Abb82376 Modified
Ade21865 HPV-16 E7
Ado05276 Human pap
Adg88451 HPV16 E7
Aao22923 Human pap
Aab31608 Amino aci
Aaw97563 Human pap
Aaw99370 Papilloma
Aab31616 Amino aci
Aay25375 HPV fusio
Aay25378 HPV fusio
Aay02631 ProtDchr1
Aay02634 Prot.D1/3

26 105 100.0 98 7 ADF18635
27 105 100.0 98 7 ADF18632
28 105 100.0 98 8 ADL90076
29 105 100.0 98 8 ADM32916
30 105 100.0 98 8 ADO44073
31 105 100.0 98 8 ADN49005
32 105 100.0 99 5 ABB81111
33 105 100.0 99 5 ABB82376
34 105 100.0 99 7 ADE21865
35 105 100.0 99 8 ADO05276
36 105 100.0 99 8 ADO88451
37 105 100.0 111 5 AAO22923
38 105 100.0 121 4 AAB31608
39 105 100.0 172 2 AAW97563
40 105 100.0 185 2 AAW99370
41 105 100.0 198 4 AAB31616
42 105 100.0 220 2 AAY25375
43 105 100.0 220 2 AAY25378
44 105 100.0 220 2 AAY02631
45 105 100.0 220 2 AAY02634

CC premalignancy, especially carcinoma by using peptides derived from the E6
 CC or E7 regions, since E6 and E7 are thought to be tumour-specific
 CC antigens. The peptides and diagnostic method are especially useful to
 CC diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix)
 CC and any HPV associated epithelial cell abnormality including high grade
 CC dysplasias, kollocytosis, hyperkeratosis, precancerous conditions
 CC encompassing intraepithelial neoplasias or intraepithelial lesions, and
 CC invasive or malignant cancers. They are also used to detect head and neck
 CC cancers, small cell lung cancers, penial and anal squamous cell carcinomas
 CC and melanoma. This is the amino acid sequence of peptide epitope #2,
 CC derived from the E7 early coding region of HPV 16, an oncoprotein that
 CC destabilises cell cycle control through its interaction with the cyclin-
 CC dependent kinase inhibitor protein, p21, described in the method of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 105; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
 |||||
 DB 1 CDSTLRLCVQSTHVDIRTLE 20
 |||||

RESULT 2
 AAR15575
 ID AAR15575 standard; protein; 30 AA.

AC AAR15575;
 DT 02-MAR-1992 (first entry)
 DE Immunopeptide #8 derived from HPV16 E7 peptide.
 XX
 KW cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
 KW squamous cell carcinoma; ELISA; HPV 16.
 XX
 OS Synthetic.

PN WO9118294-A.
 XX
 PD 28-NOV-1991.

PF 11-MAY-1990; 90SE-00001705.
 XX
 PR 11-MAY-1990; 90SE-00001705.
 XX

PA (MEDS-) MEDSCAND AB.

PI Dillner J, Dillner L, Cheng HM;
 XX
 DR WPI; 1991-369390/50.

PT Diagnosis of human papilloma virus infection and PV-carrying tumours -
 PT using synthetic peptide(s) to detect virus specific antigen-antibody
 PT complexes by immunoassay.
 XX

PS Disclosure; Page 38; 72pp; English.

XX
 CC This is one of two peptides which have been synthesised on the basis of
 CC the amino acid sequence for the E7 protein of HPV 16. The selection of
 CC peptide sequences was based on the assumption that an immunoreactive
 CC region might be situated in the same relative region of a protein from
 CC different HPV types. The peptides were used in diagnostic immunoassays to
 CC detect HPV-infection. See AAR15523-R15601
 XX

SQ Sequence 30 AA;

Query Match 100.0%; Score 105; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 9.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
 |||||
 DB 4 CDSTLRLCVQSTHVDIRTLE 23
 |||||

RESULT 3
 AAW93290

ID AAW93290 standard; peptide; 30 AA.

AC AAW93290;

DT 27-MAY-1999 (first entry)

DE Human papillomavirus peptide fragment #4.

KW Diagnosis; skin; immune reaction; onco-protein; E6; E7.

OS Human papillomavirus.

PN DE19737409-A1.

PD 04-MAR-1999.

PF 27-AUG-1997; 97DE-01037409.

PR 27-AUG-1997; 97DE-01037409.

PA (MEDI-) MEDIGENE AG.

PI Hoepfl R;

DR WPI; 1999-168276/15.

PT Diagnosis kit for testing skin for immune reactions against onco-protein
 PT E6 and E7 - comprises onco-protein E6 and E7 and/or immunologically
 PT active parts of E6 and E7 derived from human papilloma virus.

PS Disclosure; Col 3; 4pp; German.

CC This invention describes peptides used in a diagnosis kit for testing
 CC skin for immune reactions against onco-protein E6 and E7. The method of
 CC the invention comprises onco-protein E6 and E7 and/or immunologically
 CC active parts of E6 and E7 derived from human papilloma virus

SQ Sequence 30 AA;

Query Match 100.0%; Score 105; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 9.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
 |||||
 DB 1 CDSTLRLCVQSTHVDIRTLE 20
 |||||

RESULT 4
 AAO16632

ID AAO16632 standard; peptide; 50 AA.

AC AAO16632;

DT 15-MAY-2003 (first entry)

DE Human papillomavirus E7 antigen-related peptide #2.

XX Epitope; E7 antigen; CD4-positive T cell activation;
 XX uterine cancer lesion.

OS Unidentified.

PN WO2002100889-A1.

XX

PD 19-DEC-2002.
 XX
 PF 10-JUN-2002; 2002WO-JP005747.
 XX
 PR 08-JUN-2001; 2001JP-00173803.
 XX
 PA (KIRI) KIRIN BEER KK.
 XX
 PI Maeda H, Okubo M;
 XX
 DR WPI; 2003-156946/15.
 XX
 XX Novel epitope of human papilloma virus E7 antigen capable of activating
 PT CD4-positive T cells specific to (pre-)uterine cancer lesion, applicable
 PT in drug compositions for preventing and treating uterine cancer.
 XX
 PS Example 4; Page 16; 40pp; Japanese.
 XX
 CC The invention comprises an epitope of the human papillomavirus E7 antigen
 CC that is capable of activating CD4-positive T cells that are specific to
 CC uterine cancer lesions. The epitope of the invention is useful for
 CC preventing and treating uterine cancer. The present amino acid sequence
 CC represents a peptide that was used in an example of the invention
 XX
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 105; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDSTLRLCVQSTHVDIRTLE 20
 DB 13 CDSTLRLCVQSTHVDIRTLE 32
 RESULT 5
 ADF74305
 ID ADF74305 standard; protein; 92 AA.
 XX
 AC ADF74305;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human papillomavirus-16 (HPV-16) E7 delta21-26 mutant protein.
 XX
 DE mutein; human papillomavirus-16; HPV-16; E7; HPV-16 E7 delta21-26;
 KW mutant; humoral; cellular response; immunosuppressive; vaccine; cancer;
 KW tumour development.
 XX
 OS Synthetic.
 OS Human papillomavirus type 16.
 XX
 PN WO2003090664-A2.
 XX
 PD 06-NOV-2003.
 XX
 PF 24-APR-2003; 2003WO-BE000073.
 XX
 PR 24-APR-2002; 2002FR-00005173.
 PR 13-SEP-2002; 2002US-0410461P.
 PR 03-APR-2003; 2003FR-00004170.
 XX
 XX (ULBR) UNIV LIBRE BRUXELLES.
 PA
 XX Hallex S, Burny A, Jacquet A, Bollen A;
 PI
 XX WPI; 2003-865511/80.
 DR N-PSDB; ADF74304.
 DR
 XX New mutated human papillomavirus-16 E7 polypeptide having a deleted
 PT sequence from amino acid 21 to 26, useful for manufacturing a medicament
 PT in the treatment or prevention of cancer, preferably cancer induced by a
 PT human papillomavirus.

XX Claim 1; SEQ ID NO 2; 39pp; English.
 PS
 CC This invention relates to a novel mutated human papillomavirus-16 (HPV-
 CC 16) E7 polypeptide and the pharmaceutical compositions derived thereof.
 CC Specifically, it refers to the HPV-16 E7 delta21-26 mutant (residues 21-
 CC 26 have been deleted), which induces a specific humoral and cellular
 CC response against infectious agents, and furthermore can reduce or block
 CC the immunosuppressive characteristics of the native HPV-16 E7 protein.
 CC The present invention also describes a fusion protein consisting of HPV-
 CC 16 E7 delta21-26 with an HIV tat polypeptide, and inhibitors directed
 CC against these proteins such as antibodies, antisense RNA oligos or
 CC ribozymes that can block expression. Accordingly, various pharmaceutical
 CC compositions or vaccines can be derived that are useful for the
 CC manufacture of a medicament for the treatment and/or prevention of
 CC cancer and tumour development, preferably a cancer induced by a human
 CC papillomavirus, especially the strain of HPV-16. This polypeptide
 CC sequence is the recombinant HPV-16 E7 delta21-26 mutant protein of the
 CC invention.
 XX
 SQ Sequence 92 AA;
 Query Match 100.0%; Score 105; DB 7; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDSTLRLCVQSTHVDIRTLE 20
 DB 55 CDSTLRLCVQSTHVDIRTLE 74
 RESULT 6
 AAR22767
 ID AAR22767 standard; peptide; 98 AA.
 XX
 AC AAR22767;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-SEP-1992 (first entry)
 XX
 DE HPV E7 peptide.
 XX
 KW Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9205248-A.
 XX
 PD 02-APR-1992.
 XX
 PF 26-SEP-1991; 91WO-US007081.
 XX
 PR 26-SEP-1990; 90US-00588384.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;
 PI WPI; 1992-132119/16.
 DR
 XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
 PT recombinant calls encoding them, useful in treatment and prophylaxis of
 PT cervical warts or cancer resulting from HPV infection.
 XX
 XX Disclosure; Fig 7; 81pp; English.
 XX
 PS The peptide is the sequence of the human papillomavirus HPV 16 E7
 CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
 CC of HPV 16 E7 were synthesised by standard Merrifield synthesis. Examples
 CC of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these
 CC peptides, antibodies against the peptides, or recombinant cells contg.
 CC the gene encoding the immunogenic peptides may be utilised in methods for

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CC inhibiting and treating HPV infection and tumour initiation and
 CC progression e.g. in the prevention or retardation of cervical warts and
 CC cervical carcinoma resulting from HPV infection. See also AAR22766.
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 105; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 1 CDSTRLRCVQSTHVDITL 20
 |||||
 Db 61 CDSTRLRCVQSTHVDITL 80

RESULT 7
 AAR42361
 ID AAR42361 standard; protein; 98 AA.

XX AAR42361;
 XX 25-MAR-2003 (revised)
 DT 21-MAY-1994 (first entry)
 XX Human papillomavirus 16 E7 protein and fragments.
 DE
 XX Tumours; cows; horses; donkeys; regression; udder warts; HPV16.
 KW
 XX Synthetic.

XX WO9320844-A1.
 XX 28-OCT-1993.
 XX 01-APR-1993; 93WO-GB000679.
 XX 08-APR-1992; 92GB-00007701.
 XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX Camp MS;
 XX WPI; 1993-351368/44.
 DR Use of papilloma-virus E7 protein or fragments for the therapy of
 XX papilloma-virus disease - for the regression of tumours e.g. removal of
 PT warts from udders or mouth of milking cows or for treatment of horses or
 PT donkeys.

XX Disclosure; Fig 2; 31pp; English.
 PS The sequence is that of the human papillomavirus type 16 E7 protein. The
 XX protein sequence was aligned with that of bovine papillomavirus type 4.
 CC See also AAR42360. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 105; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 1 CDSTRLRCVQSTHVDITL 20
 |||||
 Db 61 CDSTRLRCVQSTHVDITL 80

RESULT 8
 AAW46886
 ID AAW46886 standard; protein; 98 AA.
 XX
 AC AAW46886;

XX 25-MAR-2003 (revised)
 DT 15-JUN-1998 (first entry)
 XX Amino acid sequence of the HPV-16 E7 oncoprotein.
 DE
 XX E7 oncoprotein; proliferative state; HPV; kinase activity;
 KW cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;
 KW cyclin/cyclin-dependent kinase inhibitor.
 XX

XX Human papillomavirus.
 OS US5736318-A.
 XX
 PN 07-APR-1998.
 XX 17-MAR-1995; 95US-00406248.
 XX 17-MAR-1995; 95US-00406248.
 XX (HARD) UNIV HARVARD.
 PA (HARD) HARVARD COLLEGE.
 PA Muenger K, Jones DL;
 XX WPI; 1998-239202/21.
 XX N-PSDB; AAV16717.

XX Evaluation of proliferative state of cells transformed with human
 PT papilloma virus - by determining cyclin-dependent kinase activity induced
 PT by E7 onco-protein.
 XX Disclosure; Col 19-20; 14pp; English.
 PS
 XX The present sequence represents Human papillomavirus (HPV), strain 16, E7
 CC oncoprotein. The proliferative state of a cell transformed with HPV can
 CC be evaluated in the following manner. Cyclin/cyclin-dependent kinase
 CC complexes containing protein p21CIP1 (AAW46887-88) are isolated from the
 CC transformed cell, and the HPV E7 oncoprotein added to the isolated
 CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an
 CC untransformed cell that is substantially homogenic with the transformed
 CC cell, and the HPV E7 oncoprotein added. The kinase activities of the 2
 CC samples are measured, where a proliferating transformed cell has a
 CC greater kinase activity than the untransformed cell. The method is used
 CC for determining the extent of interaction and/or inactivation between a
 CC cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and
 CC thus evaluating the proliferative state of a transformed cell. (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 105; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 1 CDSTRLRCVQSTHVDITL 20
 |||||
 Db 61 CDSTRLRCVQSTHVDITL 80

RESULT 9
 AAY08020
 ID AAY08020 standard; protein; 98 AA.

XX AAY08020;
 AC
 XX 27-AUG-2003 (revised)
 DT 08-JUL-1999 (first entry)
 XX Human papilloma virus E7 protein.
 XX Li protein; capsomer; virus; vaccine; infection; treatment; prevention;
 KW cervical carcinoma; fusion protein; anti-capsid; antibody; E7 protein;
 KW

KW antigenicity.
 OS Human papillomavirus.
 XX
 PN WO9918220-A1.
 XX
 PD 15-APR-1999.
 XX
 PF 06-OCT-1998; 98WO-US020965.
 XX
 XX 06-OCT-1997; 97US-00944368.
 XX
 PA (LOYO) UNIV LOYOLA CHICAGO.
 XX
 PI Gissmann L, Mueller M;
 XX
 XX WPI: 1999-264026/22.
 DR N-PSDB; AAX37567.
 XX
 XX Human papilloma virus (HPV) L1 fusion protein capsomers, used in vaccines
 PT against HPV infection.
 PT
 PS Disclosure; Page 33; 48pp; English.
 XX
 CC This invention describes novel vaccines comprising a human papilloma
 CC virus (HPV) capsomer, composed of a HPV L1 fusion protein or a HPV L1
 CC truncated protein. The vaccines can prevent or treat human papilloma
 CC virus infection. Such therapeutic vaccinations can be used for relief
 CC against, e.g. cervical carcinoma. Construction of chimeric proteins
 CC comprising amino acid residues from L1 protein, and e.g. E6 or E7
 CC protein, which give rise to chimeric capsomers, combines prophylactic and
 CC therapeutic functions of a vaccine. Capsomers can promote elimination of
 CC persistently infected cells. Capsomers can also escape neutralization by
 CC pre-existing anti-capsid antibodies and hence possess longer circulating
 CC half-life as compared to chimeric virus-like particles. The fusion
 CC protein, which forms the capsomer, provides increased antigenicity.
 CC (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 105; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDSTRLCVCQSTHVDIRTLE 20
 DB 61 CDSTRLCVCQSTHVDIRTLE 80
 RESULT 10
 AAY58474
 ID AAY58474 standard; protein; 98 AA.
 AC AAY58474;
 XX
 XX 10-APR-2000 (first entry)
 DT
 DE Human papillomavirus (HPV) E7 oncoprotein.
 XX
 XX HPV E7 oncoprotein; proteasome activity; degradation; virus component;
 KW viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
 KW virucide.
 XX
 OS Human papillomavirus.
 XX
 XX WO9966065-A2.
 PN
 XX 23-DEC-1999.
 PD
 XX 10-JUN-1999; 99WO-GB001840.
 PF
 XX 13-JUN-1998; 98GB-00012756.
 PR 13-JUN-1998; 98GB-00012757.

PR 13-JUN-1998; 98GB-00012758.
 PR 13-JUN-1998; 98GB-00012759.
 PR 13-JUN-1998; 98GB-00012760.
 XX
 PA (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.
 XX
 XX Schmid H, Petit F, Kloetzel P, Jarrousse A, Gautier K, Badaoui S;
 PI Mouzeyar S, Nicolas P;
 XX
 XX WPI: 2000-106109/09.
 DR
 XX Novel assay methods for identifying compounds which modulate and/or
 PT regulate proteosomal activity.
 PT
 XX Disclosure; Page 8; 35pp; English.
 XX
 CC The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteosomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteosomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral gene
 CC product, and protein or peptide substrates; measuring protease activity;
 CC and identifying the compound as an inhibitor if the protease activity of
 CC the assay system is increased. The assays of the invention can be used to
 CC identify compounds which inhibit viral replication and pathogenesis, and
 CC modulate and/or regulate proteasome activity. Compounds which increase
 CC proteosomal degradation of viral components or molecules induced by viral
 CC infection are of value in the treatment of viral disease. Compounds which
 CC modulate proteosomal nuclease activity have use in the treatment of
 CC inflammatory disease, and AIDS in HIV infected patients. The methods may
 CC also be used to generate resistance to bacterial or viral damage.
 CC Sequences AAY58472-Y58474 represent examples of viral proteins which
 CC affect proteosomal function
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 105; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDSTRLCVCQSTHVDIRTLE 20
 DB 61 CDSTRLCVCQSTHVDIRTLE 80
 RESULT 11
 AAY50703
 ID AAY50703 standard; protein; 98 AA.
 XX
 XX AAY50703;
 XX
 XX 04-FEB-2000 (first entry)
 DT
 DE HPV16 E7 protein.
 XX
 XX E7 protein; immunogenic; active immunization.
 KW
 XX Human papillomavirus.
 OS
 XX WO9955876-A2.
 PN
 XX 04-NOV-1999.
 PD
 XX 30-APR-1999; 99WO-DE001331.
 PF
 XX 30-APR-1998; 98DE-01019476.
 PR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Gissmann L, Jochmus I;
 PI
 XX WPI: 2000-023362/02.
 DR N-PSDB; AAZ24129.
 DR

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CC severity of disease caused by the papillomavirus is dependent on the
 CC strain causing the infection. The present sequence represents the human
 CC papillomavirus 16 E7 protein

XX Immunogenic protein with altered biological function, useful for active
 PT immunization.
 PS Example 1; Page 25; 33pp; German.
 XX This invention describes the construction of a novel polypeptide with
 XX immunogenic and altered biological function of a protein, where the
 CC immunogenic has regions of about 10-40 amino acids in a
 CC polypeptide has regions of the protein of about 10-40 amino acids in a
 CC different order. The polypeptide, or its DNA, is useful for active
 CC immunization without cross-reactivity and problems associated with the
 CC immunization of the protein. This sequence represents the human
 CC papillomavirus type 16 E7 protein which is used to illustrate the method
 CC of the invention

XX Sequence 98 AA; 100.0%; Score 105; DB 3; Length 98;
 PT Best Local Similarity 100.0%; Pred. No. 3.6e-09; Gaps 0;
 PS Matches 20; Conservative 0; Mismatches 0; Indels 0

QY 1 CDSTRLCVCVSTHVDITLLE 20
 DB 61 CDSTRLCVCVSTHVDITLLE 80

RESULT 12
 AAY57721 standard; protein; 98 AA.

XX ID AAY57721 standard; protein; 98 AA.
 XX AC AAY57721;
 XX 14-MAR-2000 (first entry)
 XX Human papillomavirus 16 E7 protein SEQ ID NO:4.
 XX Human papillomavirus; HPV; I1 fusion protein; vaccine; cytostatic;
 XX viral capsomere; virucide; dermatological; malignant tumour formation;
 XX cervical cancer; cervical intraepithelial neoplasia; genital wart;
 XX condylomata acuminata.
 XX Human papillomavirus.

XX CA2229955-A1.
 XX 20-AUG-1999.
 XX 20-FEB-1998; 98CA-02229955.
 XX 20-FEB-1998; 98CA-02229955.
 XX (MEDI-) MEDIGENE GMBH.
 XX Burger A, Hallek M;
 XX WPI; 2000-063092/06.
 XX N-PSDB; AA248175.
 XX Fusion proteins comprising papillomavirus specific proteins useful for
 XX vaccinating against malignant tumors of the anogenital tract such as
 XX cervical carcinomas.
 XX Example 1; Page 34; 45pp; English.

XX The present invention describes a fusion protein comprising 2 amino acids
 XX sequences from 2 different papillomavirus specific (PVS) proteins. The
 XX fusion protein may be administered for preventing and treating
 XX papillomavirus infections in humans and animals. Papillomaviruses are
 XX implicated in the pathology of malignant tumour formation in the
 XX anogenital tract (of these tumours, cervical cancer is the most frequent
 XX (500000 cases/year) and in the formation of precursor lesions of cervical
 XX intraepithelial neoplasia (CIN). Papillomaviruses also cause benign
 XX genital warts such as condylomata acuminata. However, the type and

XX Sequence 98 AA; 100.0%; Score 105; DB 3; Length 98;
 PT Best Local Similarity 100.0%; Pred. No. 3.6e-09; Gaps 0;
 PS Matches 20; Conservative 0; Mismatches 0; Indels 0

QY 1 CDSTRLCVCVSTHVDITLLE 20
 DB 61 CDSTRLCVCVSTHVDITLLE 80

RESULT 13
 AAB98421 standard; protein; 98 AA.

XX ID AAB98421 standard; protein; 98 AA.
 XX AC AAB98421;
 XX 22-AUG-2001 (first entry)
 XX Human papillomavirus protein HPV16 E7.
 XX Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
 XX epitope; T cell; identification; vaccine; infection; genital wart;
 XX neoplastic growth; antiviral.
 XX Human papillomavirus.
 XX WO200141799-A1.
 XX 14-JUN-2001.
 XX 11-DEC-2000; 2000WO-US033549.
 XX 10-DEC-1999; 99US-0172705P.
 XX 15-AUG-2000; 2000US-00641528.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
 XX WPI; 2001-381497/40.
 XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
 XX treating HPV infections.

XX Disclosure; Page 21; 756pp; English.

XX The present invention describes an isolated prepared human papillomavirus
 XX (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
 XX production. Peptides and corresponding nucleic acid compositions from HPV by
 XX present invention are useful for stimulating an immune response to HPV by
 XX stimulating the production of CTL or HTL responses, specifically in the
 XX treatment or prophylaxis of HPV infection, in persons who have not
 XX manifested symptoms e.g. genital warts or neoplastic growth. The peptides
 XX can also be used in a tetramer staining assay to assess peripheral blood
 XX mononuclear cells for the presence of antigen-specific CTLs following
 XX exposure to a pathogen or immunogen, and as reagents to evaluate immune
 XX recall responses or evaluate the efficacy of a vaccine. The vaccine
 XX compositions are useful for removing warts or treating HPV infections.
 XX The epitopes for inclusion in an epitope-base vaccine may be selected
 XX from conserved regions of viral or tumour-associated antigens, which
 XX reduces the likelihood of escape mutants, also immunosuppressive epitopes
 XX that may be present in whole antigens can be avoided with the use of
 XX epitope-base vaccines. An additional advantage is the ability to combine
 XX selected epitopes (CTL and HTL) and to modify the composition of the
 XX epitopes achieving enhanced immunogenicity, the major benefit of the
 XX vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
 XX polypeptide sequences used in the exemplification of the present
 XX invention

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OM protein - protein search, using sw model

Run on: January 5, 2005, 11:07:41 ; Search time 189 Seconds
(without alignments)
60.886 Million cell updates/sec

Title: US-10-827-083-4

Perfect score: 105

Sequence: 1 CDSTLRLCVQSTHVDIRTLE 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	93	2 Q9QDH2	Q9qdh2 human papil
2	105	100.0	93	2 Q9QDH4	Q9qdh4 human papil
3	105	100.0	93	2 Q9QDH6	Q9qdh6 human papil
4	105	100.0	93	2 Q9QDH8	Q9qdh8 human papil
5	105	100.0	94	2 Q8B5F6	Q8b5f6 human papil
6	105	100.0	98	1 VE7 HPV16	P03129 human papil
7	105	100.0	98	2 O11650	O11650 human papil
8	105	100.0	98	2 O12337	O12337 human papil
9	105	100.0	98	2 Q778H3	Q778h3 human papil
10	105	100.0	98	2 Q778H5	Q778h5 human papil
11	105	100.0	98	2 Q8QRD2	Q8qrd2 human papil
12	105	100.0	98	2 Q8QRD3	Q8qrd3 human papil
13	105	100.0	98	2 CAB45382	Cab45382 human pap
14	105	100.0	98	2 CAB45105	Cab45105 human pap
15	105	100.0	98	2 CAB45107	Cab45107 human pap
16	105	100.0	98	2 CAB45109	Cab45109 human pap
17	105	100.0	98	2 CAB45111	Cab45111 human pap
18	105	100.0	98	2 CAB45113	Cab45113 human pap
19	105	100.0	98	2 CAB45115	Cab45115 human pap
20	105	100.0	98	2 CAB45121	Cab45121 human pap
21	105	100.0	98	2 CAB45123	Cab45123 human pap
22	105	100.0	98	2 CAB45125	Cab45125 human pap
23	105	100.0	98	2 CAB45127	Cab45127 human pap
24	105	100.0	98	2 CAB45129	Cab45129 human pap
25	105	100.0	98	2 CAB45131	Cab45131 human pap
26	105	100.0	98	2 AAD33253	Aad33253 human pap
27	105	100.0	98	2 AAL96633	Aal96633 human pap
28	105	100.0	98	2 AAL96640	Aal96640 human pap
29	105	100.0	98	2 AAL96642	Aal96642 human pap
30	105	100.0	98	2 AAL96644	Aal96644 human pap
31	105	100.0	98	2 AAL96645	Aal96645 human pap

32	105	100.0	98	2 AAL96646	Aal96646 human pap
33	105	100.0	98	2 AAL96647	Aal96647 human pap
34	105	100.0	98	2 AAL96648	Aal96648 human pap
35	105	100.0	98	2 AAL96652	Aal96652 human pap
36	105	100.0	98	2 AAL96653	Aal96653 human pap
37	105	100.0	98	2 AAL96654	Aal96654 human pap
38	105	100.0	98	2 AAL96657	Aal96657 human pap
39	105	100.0	98	2 AAM74160	Aam74160 human pap
40	105	100.0	98	2 AAM11876	Aam11876 human pap
41	105	100.0	98	2 AAM11878	Aam11878 human pap
42	105	100.0	98	2 AAM11880	Aam11880 human pap
43	105	100.0	98	2 AAM11882	Aam11882 human pap
44	105	100.0	98	2 AAM11884	Aam11884 human pap
45	105	100.0	98	2 AAO15698	Aao15698 human pap

ALIGNMENTS

RESULT 1

Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 105; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
Db |||||
61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 2

Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 105; DB 2; Length 93;

us-10-827-083-4.rup

Wed Jan 5 11:45:33 2005

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AC Q8B5P6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment). 16.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002); to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 94 94
FT SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;
SQ
Query Match 100.0%; Score 105; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRCLCVQSTHVDIRTL 20
DB 61 CDSTLRCLCVQSTHVDIRTL 80

RESULT 3
ID Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999); to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 93 93
FT SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;
SQ
Query Match 100.0%; Score 105; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRCLCVQSTHVDIRTL 20
DB 61 CDSTLRCLCVQSTHVDIRTL 80

RESULT 4
ID Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999); to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 93 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
SQ
Query Match 100.0%; Score 105; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRCLCVQSTHVDIRTL 20
DB 61 CDSTLRCLCVQSTHVDIRTL 80

RESULT 5
ID Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment). 16.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002); to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 94 94
FT SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;
SQ
Query Match 100.0%; Score 105; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRCLCVQSTHVDIRTL 20
DB 61 CDSTLRCLCVQSTHVDIRTL 80

FUNCTION.
MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -!- SIMILARITY: LOCAL WITH ADENOVIRUS E1A AND SV40 LT.
```

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CC -----
CC EMBL; K02718; AAA46940.1; -
DR EMBL; D00735; BAA00633.1; -
DR EMBL; U76411; AAB18962.1; -
DR EMBL; U76412; AAB18963.1; -
DR EMBL; U76413; AAB18964.1; -
DR EMBL; AF003020; AAB70737.1; -
DR EMBL; AF003023; AAB70740.1; -
DR EMBL; AF003024; AAB70741.1; -
DR EMBL; AF003025; AAB70742.1; -
DR EMBL; AF003026; AAB70743.1; -
DR F1R; A03688; W7MLHS.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 105; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITL 20
DB |||||
61 CDSTLRLCVQSTHVDITL 80

RESULT 7
O11650 PRELIMINARY; PRT; 98 AA.
ID O11650; PRT; 98 AA.
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
RT from cervical cancerous and noncancerous lesions of Korean women.";
RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF534061; AAQ10404.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITL 20
DB |||||
61 CDSTLRLCVQSTHVDITL 80

RESULT 8
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ID O12337;
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITL 20
DB |||||
61 CDSTLRLCVQSTHVDITL 80

RESULT 9
O12337 PRELIMINARY; PRT; 98 AA.
ID O12337;
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITL 20
DB |||||
61 CDSTLRLCVQSTHVDITL 80

RESULT 9
O12337 PRELIMINARY; PRT; 98 AA.
ID O12337;
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

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OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RA "Analysis of human papillomavirus type 16 E6 variants in relation to
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT P53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RL EMBL; AJ388063; CAB45117.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 98 AA; 10995 MW; 81E53B534CC3281B CRC64;
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CDSTLRVCVQSTHVDIIRTLE 20
DB 61 CDSTLRVCVQSTHVDIIRTLE 80

RESULT 10
Q778H5 PRELIMINARY; PRT; 98 AA.
ID Q778H5
AC Q778H5; 2004 (TrEMBLrel. 27, Created)
DT 03-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Human papillomavirus type 16.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RA "Analysis of human papillomavirus type 16 E6 variants in relation to
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT P53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RL EMBL; AJ388062; CAB45117.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 98 AA; 10995 MW; 81E53B534CC3281B CRC64;
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CDSTLRVCVQSTHVDIIRTLE 20
DB 61 CDSTLRVCVQSTHVDIIRTLE 80

RESULT 11
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ID Q8QRD2
AC Q8QRD2; 2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.

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OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RA "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RL EMBL; AF486345; AAL96650.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;
SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CDSTLRVCVQSTHVDIIRTLE 20
DB 61 CDSTLRVCVQSTHVDIIRTLE 80

RESULT 12
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ID Q8QRD3
AC Q8QRD3; 2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RA "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RL EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CDSTLRVCVQSTHVDIIRTLE 20
DB 61 CDSTLRVCVQSTHVDIIRTLE 80

RESULT 13
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ID CAB45382
AC CAB45382; 2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OS Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX NCBI_TaxID=10581;
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.

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RC STRAIN=ET182G;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of Human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ242681; CAB45382.1; -.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
DB 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 14
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ID CAB45105 PRELIMINARY; PRT; 98 AA.
AC CAB45105;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EA7768T;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of Human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45105.1; -.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
DB 61 CDSTLRLCVQSTHVDIRTLE 80

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ID CAB45107 PRELIMINARY; PRT; 98 AA.
AC CAB45107;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX NCBI_TaxID=10581;
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RP SEQUENCE FROM N.A.
RC STRAIN=EG169G;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of Human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388057; CAB45107.1; -.

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Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CDSTLRLCVQSTHVDIRTLE 80

Search completed: January 5, 2005, 11:19:45
Job time : 189 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 5, 2005, 11:19:53 ; Search time 141 Seconds
(without alignments)
51.025 Million cell updates/sec

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Perfect score: 105
Sequence: 1 CDSTLRLCVQSTHVDIRTLE 20

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Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	105	100.0	20	10 US-09-828-645-4	Sequence 4, Appli
2	105	100.0	98	9 US-09-728-466-1	Sequence 1, Appli
3	105	100.0	98	9 US-09-820-765-4	Sequence 4, Appli
4	105	100.0	98	9 US-09-824-017-4	Sequence 4, Appli
5	105	100.0	98	10 US-09-986-118A-4	Sequence 4, Appli
6	105	100.0	98	14 US-10-267-311-8	Sequence 8, Appli
7	105	100.0	98	14 US-10-177-390-8	Sequence 8, Appli
8	105	100.0	98	14 US-10-201-764-19	Sequence 19, Appli
9	105	100.0	98	15 US-10-654-129-4	Sequence 4, Appli
10	105	100.0	98	15 US-10-681-410-19	Sequence 19, Appli
11	105	100.0	98	16 US-10-772-988-3	Sequence 3, Appli
12	105	100.0	98	16 US-10-479-541-5	Sequence 5, Appli
13	105	100.0	99	15 US-10-115-440-7	Sequence 7, Appli

14	105	100.0	111	16	US-10-472-724-4	Sequence 4, Appli
15	105	100.0	121	14	US-10-267-311-12	Sequence 12, Appli
16	105	100.0	198	14	US-10-267-311-35	Sequence 35, Appli
17	105	100.0	220	13	US-10-000-903-1	Sequence 1, Appli
18	105	100.0	220	13	US-10-000-903-8	Sequence 8, Appli
19	105	100.0	239	13	US-10-000-903-12	Sequence 12, Appli
20	105	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
21	105	100.0	289	15	US-10-115-440-5	Sequence 5, Appli
22	105	100.0	325	14	US-10-267-311-33	Sequence 33, Appli
23	105	100.0	324	14	US-10-267-311-25	Sequence 25, Appli
24	105	100.0	334	16	US-10-472-724-10	Sequence 10, Appli
25	105	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
26	105	100.0	390	13	US-10-000-903-14	Sequence 14, Appli
27	105	100.0	421	14	US-10-296-770-7	Sequence 7, Appli
28	105	100.0	493	14	US-10-267-311-19	Sequence 19, Appli
29	105	100.0	639	14	US-10-267-311-17	Sequence 17, Appli
30	105	100.0	641	14	US-10-267-311-51	Sequence 51, Appli
31	105	100.0	647	14	US-10-267-311-53	Sequence 53, Appli
32	105	100.0	648	14	US-10-267-311-29	Sequence 29, Appli
33	105	100.0	711	14	US-10-267-311-41	Sequence 41, Appli
34	105	100.0	724	14	US-10-267-311-45	Sequence 45, Appli
35	105	100.0	805	14	US-10-367-095-9	Sequence 9, Appli
36	105	100.0	805	15	US-10-368-046-9	Sequence 9, Appli
37	105	100.0	805	16	US-10-367-367-9	Sequence 9, Appli
38	97	92.4	98	14	US-10-392-113-29	Sequence 29, Appli
39	96	91.4	19	16	US-10-479-541-1	Sequence 1, Appli
40	91	86.7	18	14	US-10-355-268-16	Sequence 16, Appli
41	85	81.0	20	10	US-09-828-645-8	Sequence 8, Appli
42	83.5	79.5	19	9	US-09-888-721-7	Sequence 7, Appli
43	83.5	79.5	19	15	US-10-668-400-9	Sequence 9, Appli
44	82	78.1	15	16	US-10-306-541-89	Sequence 89, Appli
45	82	78.1	20	15	US-10-432-465-49	Sequence 49, Appli

ALIGNMENTS

RESULT 1
US-09-828-645-4
; Sequence 4, Application US/09828645
; Publication No. US20030027750A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; FILE REFERENCE: 146-1-002
; CURRENT APPLICATION NUMBER: US/09/828,645
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-4

Query Match 100.0%; Score 105; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CDSTLRLCVQSTHVDIRTLE 20
RESULT 2
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US2001002922A1
; GENERAL INFORMATION:

us-10-827-083-4.rapb

Wed Jan 5 11:45:32 2005

APPLICANT: Fisher, Christopher
 APPLICANT: He, Wanxia
 TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
 FILE REFERENCE: 28341/6216
 CURRENT APPLICATION NUMBER: US/09/728,466
 CURRENT FILING DATE: 2000-12-01
 PRIOR APPLICATION NUMBER: 09/382,616
 PRIOR FILING DATE: 1999-08-25
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 1
 LENGTH: 98
 TYPE: PRT
 ORGANISM: Papillomavirus sylvilagi
 US-09-728-466-1

Query Match 100.0%; Score 105; DB 9; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRCLVQSTHVDIRTLE 20
 Db 61 CDSTLRCLVQSTHVDIRTLE 80

RESULT 3
 US-09-820-765-4
 Sequence 4, Application US/09820765
 Publication No. US20020039584A1
 GENERAL INFORMATION:
 APPLICANT: BURGER, Alexander
 HALLER, Michael
 TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 FORMULATIONS AND METHODS OF USE
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARDNER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/820,765
 FILING DATE: 30-Mar-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/026,896
 FILING DATE: 20-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Sandercok, Colin G.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37067/102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-820-765-4
 Query Match 100.0%; Score 105; DB 9; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 CDSTLRCLVQSTHVDIRTLE 80
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 US-09-824-017-4
 Sequence 4, Application US/09824017
 Publication No. US2002019768A1
 GENERAL INFORMATION:
 APPLICANT: BURGER, Alexander
 HALLER, Michael
 TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 FORMULATIONS AND METHODS OF USE
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARDNER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/824,017
 FILING DATE: 03-Apr-2001
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,896
 FILING DATE: 1998-02-20
 ATTORNEY/AGENT INFORMATION:
 NAME: Sandercok, Colin G.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37067/102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-824-017-4
 Query Match 100.0%; Score 105; DB 9; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 CDSTLRCLVQSTHVDIRTLE 80
 RESULT 5
 US-09-986-118A-4
 Sequence 4, Application US/09986118A
 Publication No. US20030021806A1
 GENERAL INFORMATION:
 APPLICANT: BURGER, Alexander
 HALLER, Michael
 TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 FORMULATIONS AND METHODS OF USE
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARDNER
 STREET: 3000 K Street, N.W.

;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: U.S.A.
;/ ZIP: 20007-5109
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
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;/ FILING DATE: 07-No. US20030021806A1-2001
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 09/026,896
;/ FILING DATE: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Sandercock, Colin G.
;/ REGISTRATION NUMBER: 31,298
;/ REFERENCE/DOCKET NUMBER: 37067/102
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202) 672-5300
;/ TELEFAX: (202) 672-5399
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 98 amino acids
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;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
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US-09-986-118A-4

Query Match 100.0%; Score 105; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 6
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; Sequence 8, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8

Query Match 100.0%; Score 105; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CDSTLRLCVQSTHVDIRTLE 80

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; Sequence 8, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fragment of
; OTHER INFORMATION: human papilloma virus type 16 E7 gene
US-10-177-390-8

Query Match 100.0%; Score 105; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
|||||
DB 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 8
US-10-201-764-19
; Sequence 19, Application US/10201764
; Publication No. US20030166140A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: TBA
; CURRENT APPLICATION NUMBER: US/10/201,764
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/566,420
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-10-201-764-19

Query Match 100.0%; Score 105; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
|||||
DB 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 9
US-10-654-129-4
; Sequence 4, Application US/10654129
; Publication No. US20040081661A1

us-10-827-083-4.rapb

Wed Jan 5 11:45:32 2005

```

; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/654,129
; FILING DATE: 04-Sep-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandorcock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-654-129-4

Query Match 100.0%; Score 105; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITL 20
Db 61 CDSTLRLCVQSTHVDITL 80

RESULT 10
US-10-681-410-19
; Sequence 19, Application US/10681410
; Publication No. US20040096426A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: TBA
; CURRENT APPLICATION NUMBER: US/10/681,410
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/10/201,764
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/566,420
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-10-681-410-19

Query Match 100.0%; Score 105; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITL 20
Db 61 CDSTLRLCVQSTHVDITL 80

RESULT 11
US-10-772-988-3
; Sequence 3, Application US/10772988
; Publication No. US20040139485A1
; GENERAL INFORMATION:
; APPLICANT: Thorgeirsson, Snorri S.
; APPLICANT: Zhong, Minghuang
; TITLE OF INVENTION: CDNA ENCODING A GENE BOG (B5T OVER-EXPRESSED GENE) AND ITS PROTEI
; TITLE OF INVENTION: PRODUCT
; FILE REFERENCE: 11613.29USW1
; CURRENT APPLICATION NUMBER: US/10/772,988
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/637,746
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US99/04142
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 60/079,567
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/075,922
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-772-988-3

Query Match 100.0%; Score 105; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITL 20
Db 61 CDSTLRLCVQSTHVDITL 80

RESULT 12
US-10-479-541-5
; Sequence 5, Application US/10479541
; Publication No. US20040151723A1
; GENERAL INFORMATION:
; APPLICANT: Kirin Beer Kabushiki Kaisha
; TITLE OF INVENTION: Novel E7 antigen epitope from human papillomavirus and
; TITLE OF INVENTION: CD4+ T cells activated thereby
; FILE REFERENCE: 137240PX
; CURRENT APPLICATION NUMBER: US/10/479,541
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 173803/2001
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-479-541-5

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Query Match 100.0%; Score 105; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
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Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 13
US-10-115-440-7
; Sequence 7, Application US/10115440
; Publication No. US20040086845A1
; GENERAL INFORMATION:
; APPLICANT: WU, Tzvy-Chouu
; APPLICANT: HUNG, Chien-Fu
; TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF A
; TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN
; FILE REFERENCE: 02240-179934
; CURRENT APPLICATION NUMBER: US/10/115,440
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/281,003
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/US00/41422
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/501,097
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/421,608
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-115-440-7

Query Match 100.0%; Score 105; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
| | | | | | | | | | | | | | | | | | | | | |
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 14
US-10-472-724-4
; Sequence 4, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV B6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-4

Query Match 100.0%; Score 105; DB 16; Length 111;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
| | | | | | | | | | | | | | | | | | | | | |
Db 66 CDSTLRLCVQSTHVDIRTLE 85

RESULT 15
US-10-267-311-12
; Sequence 12, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-12

Query Match 100.0%; Score 105; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLE 20
| | | | | | | | | | | | | | | | | | | | | |
Db 84 CDSTLRLCVQSTHVDIRTLE 103

Search completed: January 5, 2005, 11:32:03
Job time : 141 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2005, 11:10:56 ; Search time 38' Seconds
(without alignments)
50.640 Million cell updates/sec

Title: US-10-827-083-4
Perfect score: 105
Sequence: 1 CDSTLRLCVQSTHVDIRTLR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	98	1 W7MLHS	E7 protein - human
2	91	86.7	99	1 W7ML35	E7 protein - human
3	81	77.1	98	1 W7ML31	E7 protein - human
4	80	76.2	99	2 S36574	E7 protein - human
5	68	64.8	98	1 W7ML58	E7 protein - human
6	66	62.9	97	1 W7ML33	E7 protein - human
7	58	55.2	98	1 W7ML6	E7 protein - human
8	56	53.3	86	2 S36533	E7 protein - human
9	56	53.3	97	2 S36516	E7 protein - human
10	54	51.4	98	1 W7ML11	E7 protein - human
11	51	48.6	95	2 S36480	E7 protein - human
12	50	47.6	106	2 S36562	E7 protein - human
13	50	47.6	113	1 W7MLR1	E7 protein - rhesu
14	49	46.7	92	1 S15622	E7 protein - human
15	49	46.7	104	2 S36545	E7 protein - human
16	47	44.8	93	1 W7ML42	E7 protein - human
17	46	43.8	103	2 S36539	E7 protein - human
18	45	42.9	92	1 S15615	E7 protein - human
19	45	42.9	98	1 W7MLC1	E7 protein - pygmy
20	45	42.9	102	2 S36492	E7 protein - human
21	44	41.9	93	2 S36474	E7 protein - human
22	44	41.9	105	2 S36528	E7 protein - human
23	43	41.0	102	2 S36486	E7 protein - human
24	42	40.0	93	1 W7ML	E7 protein - human
25	42	40.0	102	1 W7MLEP	E7 protein - Europ
26	42	40.0	251	2 H84861	3-isopropylmalate
27	42	40.0	267	1 DCBYOF	orotidine-5'-phosp
28	42	40.0	267	1 DEBYOP	orotidine-5'-phosp
29	42	40.0	338	2 T26113	hypothetical prote

ALIGNMENTS

RESULT 1

W7MLHS

E7 protein - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03688; S12367; T10428

R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Viology 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03688

A;Molecule type: DNA

A;Residues: 1-98 <SEE>

A;Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G33303

R;Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 lar

A;Reference number: S12367; MUID:90107938; PMID:2153075

A;Accession: S12367

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-98 <BAR>

R;Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10428

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-98 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

C;Genetics:

A;Gene: E7

C;Superfamily: papillomavirus E7 protein

C;Keywords: DNA binding; early protein; transcription regulation; zinc finger

F;58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 105; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 2,1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDIRTLR 20

|||||

Db 61 CDSTLRLCVQSTHVDIRTLR 80

RESULT 2

W7ML35

E7 protein - human papillomavirus type 35

C;Species: human papillomavirus type 35

A;Note: host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

A:Accession: S36574
A:Molecule type: DNA
A:Residues: 1-99
A:Cross-references: UNIPROT:P36831; EMBL:X74481; NID:g397038; PIDN:CAA52586.1; PID:g3970
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 76.2%; Score 80; DB 2; Length 99;
Best Local Similarity 70.0%; Pred. No. 3.4e-06; Indels 0; Gaps 0;
Matches 14; Conservative

QY 1 CDSTRLCVCQSTHVDIIRLQ 20
Db 63 CDSTRLCVCQSTHVDIIRLQ 82

RESULT 5
W7ML58
E7 protein - human papillomavirus type 58
C:Species: human papillomavirus type 58
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: F36779
R:Kiri, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A:Title: Human papillomavirus type 58 DNA sequence.
A:Reference number: A36779; MUID:92024102; PMID:1656594
A:Accession: F36779
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <KIR>
A:Cross-references: UNIPROT:P26557; GB:D90400; NID:g222386; PIDN:BA31846.1; PID:g333705
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 64.8%; Score 68; DB 1; Length 98;
Best Local Similarity 55.0%; Pred. No. 0.00034; Indels 0; Gaps 0;
Matches 11; Conservative

QY 1 CDSTRLCVCQSTHVDIIRLQ 20
Db 62 CGTTLRLCINSTTTVDIIRLQ 81

RESULT 6
W7ML33
E7 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03689; S23831; S23827
R:Cole, S.T.; Strecek, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33.
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03689
A:Molecule type: DNA
A:Residues: 1-97 <COL>
A:Cross-references: UNIPROT:P06429; GB:M12732; NID:g333049; PIDN:AAA46959.1; PID:g46317E
R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
submitted to the EMBL Data Library, January 1992
A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t
A:Reference number: S19906
A:Accession: S23831
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97 <SNI>
A:Cross-references: EMBL:X64085; NID:g60278; PIDN:CAA45434.1; PID:g60281; EMBL:X64084, 1
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 62.9%; Score 66; DB 1; Length 97;

C:Accession: F40824; S36522
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papill
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: F40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-99 <MAR>
A:Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999
C:Experimental source: strain 35H
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 86.7%; Score 91; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 4.8e-08; Indels 0; Gaps 0;
Matches 16; Conservative

QY 1 CDSTRLCVCQSTHVDIIRLQ 20
Db 62 CEATRLCVCQSTHVDIIRLQ 81

RESULT 3
W7ML31
E7 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: B32444
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: B32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <GOL>
A:Cross-references: UNIPROT:P17387; GB:J04353; NID:g333048; PIDN:AAA46951.1; PID:g459917
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 77.1%; Score 81; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 2.3e-06; Indels 0; Gaps 0;
Matches 16; Conservative

QY 1 CDSTRLCVCQSTHVDIIRLQ 20
Db 61 CKSTRLCVCQSTHVDIIRLQ 80

RESULT 4
S36574
E7 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S36574
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469

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A;Residues: 1-97 <DEL>
A;Cross-references: UNIPROT:P36828; EMBL:X74476; NID:g396989; PIDN:CAA52556.1; PID:g399
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 53.3%; Score 56; DB 2; Length 97;
Best Local Similarity 50.0%; Pred. No. 0.035;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITRL 20
DB 60 CQSTVCLTIESHADLLVLE 79
|||:|:|||||:|
|:|:|:|:|:|:|

RESULT 10
W7WL11
E7 protein - human papillomavirus type 11
C;Species: human papillomavirus type 11
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A03690
R;Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
Virology 151, 124-130, 1986
A;Title: The nucleotide sequence and genome organization of human papilloma virus type
A;Reference number: A94338; MUID:86181601; PMID:3008427
A;Accession: A03690
A;Molecule type: DNA
A;Residues: 1-98 <DEL>
A;Cross-references: UNIPROT:P04020; GB:M14119; NID:g333026; PIDN:AAA46928.1; PID:g49619
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

Query Match 51.4%; Score 54; DB 1; Length 98;
Best Local Similarity 55.0%; Pred. No. 0.077;
Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITRL 20
DB 61 CDSNVLVVECTDGIHQ 80
|||:|:|||||:|
|:|:|:|:|:|:|

RESULT 11
S36480
E7 protein - human papillomavirus type 17
C;Species: human papillomavirus type 17
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36480
R;Dellius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36480
A;Molecule type: DNA
A;Residues: 1-95 <DEL>
A;Cross-references: UNIPROT:P36821; EMBL:X74469; NID:g396932; PIDN:CAA52513.1; PID:g396
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 48.6%; Score 51; DB 2; Length 95;
Best Local Similarity 55.0%; Pred. No. 0.24;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CDSTLRLCVQSTHVDITRL 20
DB 55 CGSKRLIVLTHAGIRSQE 74
|||:|:|||||:|
|:|:|:|:|:|:|

RESULT 12
S36562
E7 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36562

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RESULT 15
S36545
E7 protein - human papillomavirus type 26
C/Species: human papillomavirus type 26
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36545
R/Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36545
A/Molecule type: DNA
A/Residues: 1-104 <DEL>
A/Cross-references: UNIPROT:P36824; EMBL:X74472; NID:G396956; PIDN:CAA52531
C/Superfamily: papillomavirus E7 protein
C/Keywords: DNA binding; early protein; transcription regulation

Query Match 46.7%; Score 49; DB 2; Length 104;
Best Local Similarity 45.0%; Pred. No. 0.56;
Matches 9; Conservative 6; Mismatches 5; Indels 0; Gaps

Qy 1 CDSTLRLCVQSTHVDITRL 20
|:|:| |:| |:|
Db 68 CNSIQVLAQSSRQNRVRL 87

Search completed: January 5, 2005, 11:20:30
Job time : 39 secs

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